70681

STIC-Biotech/ChemLib

184292

M

From:	Myers, Carla
Sent:	Wednesday, April 05, 2006 11:26 AM
To:	STIC-Biotech/ChemLib
Subject:	sequence search for 09/701,132

Please search:
a) an n-mer search for fragments of 10 or more nucleotides of SEQ ID NO: 13.
(i.e., the claims are limited to nucleic acids consisting of 10 or more nucleotides of SEQ ID NO: 13, so I would like to find
references that include only the sequences of SEQ ID NO: 13)

b) nucleotides 586 to 810 of SEQ ID NO: 13.

c) SEQ ID NO: 57

d) nucleotides 79 to 6471 of SEQ ID NO: 56

e) nucleotides 13261 to 13821 of SEQ ID NO: 56

Please provide a printout of the first 40 results.

Thank you

Carla Myers
AU 1634
Remsen Bldg / Rm 2E79
Mailbox: REM 2C70
571-272-0747

WEST Search History

DATE: Tuesday, June 06, 2006

Hide?	Set Name	Query	Hit Count
		DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ	
☐	L9	coli same (O adj serotype)	15
☐	L8	L7 and (pcr or primer or probe or amplifi$ or hybridi$)	342
☐	L7	(flagella or flagellin) same coli	391
☐	L6	L3 and (H or O)	337
☐	L5	L2 and ((H adj serotype) or (O adj serotype))	6
☐	L4	L3 and ((H adj serotype) or (O adj serotype))	4
☐	L3	L2 and (pcr or primers or hybridi$ or probe)	354
☐	L2	L1 same coli	405
☐	L1	flagellin or flmA or flkA or flic or fliC or flagella	2513

END OF SEARCH HISTORY

☐ gi|290160|gb|L15643.1|DOGP23602 Dog (Clone: CXX.236) primer for STS 236, 3' end
Length=22

 Score = 28.2 bits (14), Expect = 1.0
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query 1047 TGGTAACAATAAAG 1060
             ||||||||||||||
Sbjct 15   TGGTAACAATAAAG 2

> ☐ gi|29565480|emb|AJ544052.1|DME544052 Drosophila melanogaster partial snmRNA gene for s
RNA, clone Dm-173
Length=31

 Score = 26.3 bits (13), Expect = 4.0
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query 471 CGATGGCGCGCAG 483
            |||||||||||||
Sbjct 19   CGATGGCGCGCAG 31

> ☐ gi|3135150|dbj|D88711.1| Hepatitis G virus RNA for polyprotein (N3 region), partial co
isolate D77
Length=43

 Score = 26.3 bits (13), Expect = 4.0
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 357 CCTTGCTGAAAAT 369
            |||||||||||||
Sbjct 28   CCTTGCTGAAAAT 16

> ☐ gi|51947926|gb|AY733678.1| Macaca mulatta isolate 96E025-MDS1 MLV-derived vector prov:
integration site
Length=50

 Score = 24.3 bits (12), Expect =   16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 1133 CTACCACCAÁCC 1144
             ||||||||||||
Sbjct 15   CTACCACCAACC 26

> ☐ gi|255419|gb|S44672.1|S44670S2 snRNA U2-1 [Tetrahymena thermophila, Genomic, 50 nt, se
2 of 2]
Length=50

 Score = 24.3 bits (12), Expect =   16
 Identities = 15/16 (93%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

```
Query  845  ACAAAAAAGCTTCTTT  860
            ||||||||| |||||||
Sbjct   24  ACAAAAAACCTTCTTT   39
```

> ☐ gi|62816380|emb|AJ965727.1| Pisum sativum PDR1 retrotransposon partial right terminal
clone 1006-R11
Length=48

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 15/16 (93%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query  416  CTATCAATCTGGCAAA  431
            |||||||||||| ||||
Sbjct   33  CTATCAATCTGACAAA   18
```

```
 Score = 22.3 bits (11),  Expect =    62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 1256  ACAACCTGTCT  1266
            |||||||||||
Sbjct   45  ACAACCTGTCT   35
```

```
 Score = 20.3 bits (10),  Expect =   244
 Identities = 10/10 (100%), Gaps = 0/10 (0%)
 Strand=Plus/Minus

Query 1225  TCTGCTATCA  1234
            ||||||||||
Sbjct   37  TCTGCTATCA   28
```

```
 Score = 18.3 bits (9),  Expect =   965
 Identities = 9/9 (100%), Gaps = 0/9 (0%)
 Strand=Plus/Minus

Query  647  AATCTGACA  655
            |||||||||
Sbjct   28  AATCTGACA  20
```

> ☐ gi|88687633|dbj|AB251241.1| Mus musculus RNA for germline small RNA gsRNA271, complete
Length=26

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  924  CAAGGCTGCCAC  935
            ||||||||||||
Sbjct    2  CAAGGCTGCCAC   13
```

> ☐ gi|71612503|dbj|AB213806.1| Synthetic construct DNA, reverse primer for microsatellite

Length=23

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query  111  AGCAAATATTAA  122
            ||||||||||||
Sbjct  19   AGCAAATATTAA  8
```

> ☐ gi|71615529|dbj|AB213945.1| Synthetic construct DNA, forward primer for microsatellite
Length=22

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  929  CTGCCACACTTT  940
            ||||||||||||
Sbjct  4    CTGCCACACTTT  15
```

> ☐ gi|1340050|emb|Z73089.1|HSBTIII60 H.sapiens mRNA for T cell receptor beta chain V-D-J
region (BV12BJ1S1; cell line BTIII 60)
Length=45

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  173  AGACCACTGAAG  184
            ||||||||||||
Sbjct  23   AGACCACTGAAG  34
```

> ☐ gi|9963961|gb|AF246208.1|F246197S12 Rattus norvegicus mitochondrial transcription fact
VI - exon VII boundary; nuclear gene for mitochondrial product
Length=50

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  66  TGCTAAAGATGA  77
           ||||||||||||
Sbjct  38  TGCTAAAGATGA  49
```

> ☐ gi|1675337|gb|U71397.1|MMTFAM14 🇬 Mus musculus mitochondrial transcription factor A (:
nuclear gene encoding mitochondrial protein, intron 6 and
exon 7
Length=50

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  66  TGCTAAAGATGA  77
```

```
              ||||||||||||
Sbjct   35    TGCTAAAGATGA    46
```

> ☐ gi|1675329|gb|U71386.1|MMTFAM06 Ⓖ Mus musculus mitochondrial transcription factor A (ⁿ
nuclear gene encoding mitochondrial protein, exon 3 and intron
3
Length=50

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query  1040   CTGCTTCTGGTA   1051
              ||||||||||||
Sbjct   32    CTGCTTCTGGTA    21
```

> ☐ gi|425562|gb|S65766.1|S65766S1 COL4A5=type IV collagen alpha 5 chain [human, Alport sɔ
Genomic Mutant, 34 nt, segment 1 of 2]
Length=34

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  152   ATGATGGTATTT   163
             ||||||||||||
Sbjct   17   ATGATGGTATTT    28
```

```
 Score = 18.3 bits (9),  Expect =   965
 Identities = 9/9 (100%), Gaps = 0/9 (0%)
 Strand=Plus/Plus

Query  628   GATGGTTCA   636
             |||||||||
Sbjct   9    GATGGTTCA    17
```

> ☐ gi|14277086|gb|AF357491.1|AF357491 Mus musculus clone MBI-72 miscellaneous RNA, partiε
Length=48

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  641   CAACTAAATCTG   652
             ||||||||||||
Sbjct   36   CAACTAAATCTG    47
```

> ☐ gi|66353939|gb|AY227177.2| Corvus monedula opsin (SWS1) gene, partial cds
Length=50

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus
```

```
Query  1108   GAAGATGCAGCA   1119
              ||||||||||||
Sbjct  19     GAAGATGCAGCA   8
```

> ☐ gi|38423190|emb|AJ538790.1|NTA538790   Nicotiana tabacum cDNA-AFLP-fragment BT1-M24-058
Length=34

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%),  Gaps = 0/12 (0%)
 Strand=Plus/Minus


Query  1282   ATCGAAGATGCT   1293
              ||||||||||||
Sbjct  13     ATCGAAGATGCT   2
```

> ☐ gi|2564273|emb|AJ002273.1|MMAJ2273   Drosophila melanogaster troponin T gene, intron 3,
Length=43

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%),  Gaps = 0/12 (0%)
 Strand=Plus/Minus


Query  1334   TCCTGCAACAAG   1345
              ||||||||||||
Sbjct  42     TCCTGCAACAAG   31
```

> ☐ gi|154705|gb|J01816.1|TIP58CG4   Integrated Ti plasmid (from A.tumefaciens), nopaline st
clone cg4, left end of T-DNA at host DNA/T-DNA border
Length=48

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%),  Gaps = 0/12 (0%)
 Strand=Plus/Minus


Query  898    CTTTATACGACA   909
              ||||||||||||
Sbjct  12     CTTTATACGACA   1
```

> ☐ gi|51947981|gb|AY733733.1| Macaca mulatta isolate 96e025-3q26.2 MLV-derived vector pro
integration site
Length=50

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%),  Gaps = 0/12 (0%)
 Strand=Plus/Plus


Query  1133   CTACCACCAACC   1144
              ||||||||||||
Sbjct  15     CTACCACCAACC   26
```

> ☐ gi|15129391|dbj|AB068587.1| Synthetic construct DNA, reverse primer for human STS sts-
at 1p36
Length=20

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus


Query  714   AGCACAGAATGA   725
             ||||||||||||
Sbjct  7     AGCACAGAATGA   18
```

> ☐ gi|15129302|dbj|AB068498.1| Synthetic construct DNA, forward primer for human STS sts·
at 1p36
Length=19

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus


Query  845   ACAAAAAAGCTT   856
             ||||||||||||
Sbjct  6     ACAAAAAAGCTT   17
```

> ☐ gi|15128874|dbj|AB068070.1| Synthetic construct DNA, forward primer for human STS sts·
at 1p36
Length=24

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus


Query  485   AAGCAACTGGCA   496
             ||||||||||||
Sbjct  4     AAGCAACTGGCA   15
```

> ☐ gi|216228|dbj|D13786.1|BACAAMSP Bacillus subtilis gene for alpha-amylase, partial cds,
signal peptide
Length=27

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus


Query  687   AGCACTCGCAGC   698
             ||||||||||||
Sbjct  27    AGCACTCGCAGC   16
```

> ☐ gi|14586472|emb|AJ404691.1|MMU404691 Mus musculus partial mRNA for T-cell receptor al|
A4.1.E9
Length=48

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus


Query  630   TGGTTCACTGAC   641
             ||||||||||||
```

```
Sbjct  18  TGGTTCACTGAC  7
```

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus
```

```
Query  630  TGGTTCACTGAC  641
            ||||||||||||
Sbjct  18  TGGTTCACTGAC  7
```

> ☐ gi|913873|gb|S76024.1|S76024   {elementary chromomere pChM8} [mice, interphase chromosom
Genomic, 47 nt]
Length=47

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus
```

```
Query  505  ATTTCTAAATTT  516
            ||||||||||||
Sbjct  4    ATTTCTAAATTT  15
```

> ☐ gi|56966056|pdb|1T9J|D   Chain D, I-Crei(Q47e)DNA COMPLEX
Length=24

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus
```

```
Query  869  GTGAGACAGTTT  880
            ||||||||||||
Sbjct  14  GTGAGACAGTTT  3
```

> ☐ gi|56966055|pdb|1T9J|C   Chain C, I-Crei(Q47e)DNA COMPLEX
Length=24

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus
```

```
Query  869  GTGAGACAGTTT  880
            ||||||||||||
Sbjct  11  GTGAGACAGTTT  22
```

> ☐ gi|56966052|pdb|1T9I|D   Chain D, I-Crei(D20n)DNA COMPLEX
Length=24

```
 Score = 24.3 bits (12),  Expect =    16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus
```

```
Query  869  GTGAGACAGTTT  880
            ||||||||||||
Sbjct  14  GTGAGACAGTTT  3
```

> ⌐¬gi|56966051|pdb|1T9I|C Chain C, I-Crei(D20n)DNA COMPLEX
Length=24

 Score = 24.3 bits (12), Expect =   16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 869 GTGAGACAGTTT 880
            ||||||||||||
Sbjct 11   GTGAGACAGTTT 22

> □gi|55670022|pdb|1TRJ|B Chain B, Homology Model Of Yeast Rack1 Protein Fitted Into 11.7
Cryo-Em Map Of Yeast 80s Ribosome
Length=41

 Score = 24.3 bits (12), Expect =   16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 240 GGCAACTAACGG 251
            ||||||||||||
Sbjct 15   GGCAACTAACGG 4

 Score = 18.3 bits (9), Expect =   965
 Identities = 9/9 (100%), Gaps = 0/9 (0%)
 Strand=Plus/Plus

Query 980 CGTTAGTTG 988
            |||||||||
Sbjct 5   CGTTAGTTG 13

> □gi|927128|gb|L36734.1|MUSIGDJAL Mus musculus rearranged immunoglobulin heavy chain D-ί
(clone 20JH3)
Length=31

 Score = 24.3 bits (12), Expect =   16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 1271 CCCGTAGCCGTA 1282
             ||||||||||||
Sbjct 20   CCCGTAGCCGTA 9

> □gi|13786782|pdb|1G9Z|E Chain E, Laglidadg Homing Endonuclease I-Crei DNA PRODUCT COMI
With Magnesium
Length=14

 Score = 24.3 bits (12), Expect =   16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 869 GTGAGACAGTTT 880
            ||||||||||||

```
Sbjct   14   GTGAGACAGTTT   3
```

> ☐ gi|13786777|pdb|1G9Y|D   Chain D, Homing Endonuclease I-Crei   DNA SUBSTRATE COMPLEX WITH
Calcium
Length=24

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query   869   GTGAGACAGTTT   880
              ||||||||||||
Sbjct   11   GTGAGACAGTTT   22
```

> ☐ gi|13786776|pdb|1G9Y|C   Chain C, Homing Endonuclease I-Crei   DNA SUBSTRATE COMPLEX WITH
Calcium
Length=24

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query   869   GTGAGACAGTTT   880
              ||||||||||||
Sbjct   14   GTGAGACAGTTT   3
```

> ☐ gi|180740|gb|M68994.1|HUM13COL25   Human alpha-1 type XIII collagen (COL13A1) gene, exon
Length=44

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query   806   TTGATGGTAAGT   817
              ||||||||||||
Sbjct   29   TTGATGGTAAGT   40


 Score = 20.3 bits (10),  Expect =    244
 Identities = 10/10 (100%), Gaps = 0/10 (0%)
 Strand=Plus/Plus

Query   891   CGCTGGCCTT   900
              ||||||||||
Sbjct   21   CGCTGGCCTT   30
```

> ☐ gi|4139431|pdb|1BP7|4   Chain 4, Group I Mobile Intron Endonuclease I-Crei Complexed
With Homing Site Dna
Length=24

```
 Score = 24.3 bits (12),  Expect =     16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query   869   GTGAGACAGTTT   880
```

```
                    ||||||||||||
Sbjct   14   GTGAGACAGTTT    3
```

> ☐ gi|4139430|pdb|1BP7|3   Chain 3, Group I Mobile Intron Endonuclease I-Crei Complexed
With Homing Site Dna
Length=24

```
  Score = 24.3 bits (12),   Expect =    16
  Identities = 12/12 (100%), Gaps = 0/12 (0%)
  Strand=Plus/Plus
```

```
Query   869   GTGAGACAGTTT    880
                    ||||||||||||
Sbjct   11   GTGAGACAGTTT    22
```

> ☐ gi|4139429|pdb|1BP7|2   Chain 2, Group I Mobile Intron Endonuclease I-Crei Complexed
With Homing Site Dna
Length=24

```
  Score = 24.3 bits (12),   Expect =    16
  Identities = 12/12 (100%), Gaps = 0/12 (0%)
  Strand=Plus/Minus
```

```
Query   869   GTGAGACAGTTT    880
                    ||||||||||||
Sbjct   14   GTGAGACAGTTT    3
```

> ☐ gi|4139428|pdb|1BP7|1   Chain 1, Group I Mobile Intron Endonuclease I-Crei Complexed
With Homing Site Dna
Length=24

```
  Score = 24.3 bits (12),   Expect =    16
  Identities = 12/12 (100%), Gaps = 0/12 (0%)
  Strand=Plus/Plus
```

```
Query   869   GTGAGACAGTTT    880
                    ||||||||||||
Sbjct   11   GTGAGACAGTTT    22
```

> ☐ gi|88687684|dbj|AB251292.1| Mus musculus RNA for germline small RNA gsRNA322, complete
Length=25

```
  Score = 22.3 bits (11),   Expect =    62
  Identities = 11/11 (100%), Gaps = 0/11 (0%)
  Strand=Plus/Plus
```

```
Query   780   TGGGAATGGTG    790
                    |||||||||||
Sbjct   11   TGGGAATGGTG    21
```

> ☐ gi|88687467|dbj|AB251075.1| Mus musculus RNA for germline small RNA gsRNA105, complete
Length=26

```
 Score = 22.3 bits (11),  Expect =     62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus


Query  972   AGGAAGCACGT   982
             |||||||||||
Sbjct  2     AGGAAGCACGT   12
```

> ☐ gi|624799|dbj|D44509.1|BOVDIK08   Bos taurus DNA, microsatellite DIK016 PCR antisense pi
Length=20

```
 Score = 22.3 bits (11),  Expect =     62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus


Query  712   AAAGCACAGAA   722
             |||||||||||
Sbjct  4     AAAGCACAGAA   14
```

> ☐ gi|60099378|dbj|AB117772.1| Arabidopsis thaliana AT3G27920.1 gene rearrangement juncti
sequence, junction site 1, allele: gl1-3
Length=47

```
 Score = 22.3 bits (11),  Expect =     62
 Identities = 14/15 (93%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  395   CTAATGATGGTGAAA   409
             ||||||||| ||||||
Sbjct  19    CTAATGATAGTGAAA   33
```

> ☐ gi|10242157|gb|AF254841.1|AF254841   Pyrococcus abyssi box C/D small nucleolar RNA sR8
Length=50

```
 Score = 22.3 bits (11),  Expect =     62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus


Query  469   ATCGATGGCGC   479
             |||||||||||
Sbjct  19    ATCGATGGCGC   9
```

> ☐ gi|10242139|gb|AF254823.1|AF254823   Pyrococcus abyssi box C/D small nucleolar RNA sR1
Length=50

```
 Score = 22.3 bits (11),  Expect =     62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus


Query  581   GAGCTGTTAAA   591
             |||||||||||
Sbjct  11    GAGCTGTTAAA   21
```

> ☐ gi|438167|emb|Z22831.1|MMTCRVJAC   M.musculus T cell receptor V alpha 8 F3.4 and T cell J alpha TA39 mRNA
Length=39

```
 Score = 22.3 bits (11),  Expect =    62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus


Query  712  AAAGCACAGAA  722
            |||||||||||
Sbjct  14   AAAGCACAGAA  4
```


> ☐ gi|2288937|emb|AJ000950.1|SSAJ950   Sus scrofa EST 3'UTR CAP2A2 reverse primer
Length=22

```
 Score = 22.3 bits (11),  Expect =    62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus


Query  377  TGAAAATTCAG  387
            |||||||||||
Sbjct  12   TGAAAATTCAG  22
```


> ☐ gi|1107766|emb|Z49031.1|MMTCR1242   M.musculus partial gene for T cell receptor gamma-cl CR124,_2)
Length=18

```
 Score = 22.3 bits (11),  Expect =    62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus


Query  791  TATATTCTGCA  801
            |||||||||||
Sbjct  13   TATATTCTGCA  3
```


> ☐ gi|5804969|emb|AJ232730.1|MMU232730   Mus musculus mRNA for T cell receptor, clone T4.1.
Length=45

```
 Score = 22.3 bits (11),  Expect =    62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus


Query  78   CGCAGCAGGTC  88
            |||||||||||
Sbjct  3    CGCAGCAGGTC  13
```

gi|40791077|gb|CA585955.1| LBA00522.BOST4 cDNA from mouse aorta Mus musculus cDNA, mRNA
sequence.
Length=36

 Score = 32.2 bits (16), Expect = 0.24
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 796   TCTGCAGAAATTGATG   811
            ||||||||||||||||
Sbjct 20   TCTGCAGAAATTGATG   35

> ☐gi|1321007|gb|W39290.1| zc76g04.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328:
5' similar to WP:R13A5.13 CE01374 ;, mRNA sequence.
Length=49

 Score = 30.2 bits (15), Expect = 0.95
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 966   GAAAACAGGAAGCAC   980
            |||||||||||||||
Sbjct 33   GAAAACAGGAAGCAC   19

> ☐gi|458592|gb|T17570.1| mps v30 The blue guys library Saccharomyces cerevisiae cDNA se(
upstream of LacZ fusion similar to RNA12, S92205, mRNA
sequence.
Length=43

 Score = 30.2 bits (15), Expect = 0.95
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 360   TGCTGAAAATAATGA   374
            |||||||||||||||
Sbjct 17   TGCTGAAAATAATGA   3

> ☐gi|86584026|gb|DY248386.1| CSTCP1D0047A_655_691 CST-QuHSC Mus musculus cDNA, mRNA seqı
Length=36

 Score = 28.2 bits (14), Expect = 3.8
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query 799   GCAGAAATTGATGG   812
            ||||||||||||||
Sbjct 20   GCAGAAATTGATGG   7

 Score = 20.3 bits (10), Expect = 916
 Identities = 13/14 (92%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query 426   GGCAAAAATTGATG   439
            ||||| |||||||||
Sbjct 21   GGCAGAAATTGATG   8

>☐gi|598647|dbj|D17167.1| D17167 Kiseru Homo sapiens cDNA clone hmd2e06m3, mRNA sequence
Length=48

```
 Score = 28.2 bits (14),  Expect = 3.8
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus


Query  873  GACAGTTTACAAAA  886
            ||||||||||||||
Sbjct  22   GACAGTTTACAAAA  35



 Score = 20.3 bits (10),  Expect =   916
 Identities = 13/14 (92%), Gaps = 0/14 (0%)
 Strand=Plus/Minus


Query  359  TTGCTGAAAATAAT  372
            ||||  ||||||||
Sbjct  48   TTGCAGAAAATAAT  35
```

>☐gi|16838007|dbj|AV852668.1| AV852668 Nori Satoh unpublished cDNA library, egg Ciona i₁
cDNA clone rcieg23b22 3', mRNA sequence.
Length=39

```
 Score = 28.2 bits (14),  Expect = 3.8
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus


Query  396  TAATGATGGTGAAA  409
            ||||||||||||||
Sbjct  25   TAATGATGGTGAAA  38
```

>☐gi|13554728|dbj|AU105207.1| AU105207 Sugano Homo sapiens cDNA library Homo sapiens cD₁
KAT01893 5', mRNA sequence.
Length=50

```
 Score = 28.2 bits (14),  Expect = 3.8
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus


Query  19  CTGAGCTCCGCCAT  32
           ||||||||||||||
Sbjct  7   CTGAGCTCCGCCAT  20
```

>☐gi|13554727|dbj|AU105206.1| AU105206 Sugano Homo sapiens cDNA library Homo sapiens cD₁
HRC08436 5', mRNA sequence.
Length=50

```
 Score = 28.2 bits (14),  Expect = 3.8
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus


Query  19  CTGAGCTCCGCCAT  32
           ||||||||||||||
```

```
Sbjct   12  CTGAGCTCCGCCAT   25
```

>☐ gi|13554726|dbj|AU105205.1| AU105205 Sugano Homo sapiens cDNA library Homo sapiens cDN
HRC07843 5', mRNA sequence.
Length=50

```
 Score = 28.2 bits (14),  Expect = 3.8
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query   19  CTGAGCTCCGCCAT   32
            ||||||||||||||
Sbjct    6  CTGAGCTCCGCCAT   19
```

>☐ gi|13554725|dbj|AU105204.1| AU105204 Sugano Homo sapiens cDNA library Homo sapiens cDN
HRC06024 5', mRNA sequence.
Length=50

```
 Score = 28.2 bits (14),  Expect = 3.8
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query   19  CTGAGCTCCGCCAT   32
            ||||||||||||||
Sbjct    5  CTGAGCTCCGCCAT   18
```

>☐ gi|13554720|dbj|AU105199.1| AU105199 Sugano Homo sapiens cDNA library Homo sapiens cDN
HRC00642 5', mRNA sequence.
Length=50

```
 Score = 28.2 bits (14),  Expect = 3.8
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query   19  CTGAGCTCCGCCAT   32
            ||||||||||||||
Sbjct    6  CTGAGCTCCGCCAT   19
```

>☐ gi|86580324|gb|DY244680.1| CSTBQ1D0647A_0_36 CST-BM Mus musculus cDNA, mRNA sequence.
Length=36

```
 Score = 26.3 bits (13),  Expect =    15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  383  TTCAGGTTGGTGC   395
            |||||||||||||
Sbjct   32  TTCAGGTTGGTGC   20
```

>☐ gi|82861917|gb|DR980846.1| SM016930 Placenta 3' EST Homo sapiens cDNA clone ID_16930 :
mRNA sequence.
Length=44

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  161  TTTCTGTTGCGCA  173
            |||||||||||||
Sbjct  23   TTTCTGTTGCGCA  11
```

>☐ gi|82860386|gb|DR979315.1| SM014071 Placenta 3' EST Homo sapiens cDNA clone ID_14071 :
mRNA sequence.
Length=48

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  370  AATGAAATGAAAA  382
            |||||||||||||
Sbjct  30   AATGAAATGAAAA  42


 Score = 24.3 bits (12),  Expect =     59
 Identities = 15/16 (93%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  366  AAATAATGAAATGAAA  381
            ||||  ||||||||||||
Sbjct  21   AAATGATGAAATGAAA  36
```

>☐ gi|67225679|dbj|BP915998.1| BP915998 Adiantum capillus-veneris prothallium Adiantum ca
cDNA clone YMU001_000081_F12, mRNA sequence.
Length=46

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  349  GTGAAAGTCCTTG  361
            |||||||||||||
Sbjct  9    GTGAAAGTCCTTG  21
```

>☐ gi|33679581|gb|CF307820.1| ABF--01-G06.g1 ABF3-overexpressing transgenic rice plasmid
library (ABF) Oryza sativa (japonica cultivar-group) cDNA
clone ABF--01-G06, mRNA sequence.
Length=39

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1130  AATCTACCACCAA  1142
             |||||||||||||
Sbjct  1     AATCTACCACCAA  13
```

>☐ gi|33679580|gb|CF307819.1| ABF--01-G06.b1 ABF3-overexpressing transgenic rice plasmid

library (ABF) Oryza sativa (japonica cultivar-group) cDNA
clone ABF--01-G06, mRNA sequence.
Length=39

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus


Query  1130   AATCTACCACCAA  1142
              |||||||||||||
Sbjct  39     AATCTACCACCAA  27
```


> ☐ gi|33674726|gb|CF302965.1| 7LEAF--08-P09.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-P09,
mRNA sequence.
Length=47

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus


Query  1130   AATCTACCACCAA  1142
              |||||||||||||
Sbjct  47     AATCTACCACCAA  35
```


> ☐ gi|33672814|gb|CF301053.1| 7LEAF--05-M03.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M03,
mRNA sequence.
Length=48

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus


Query  1130   AATCTACCACCAA  1142
              |||||||||||||
Sbjct  48     AATCTACCACCAA  36
```


> ☐ gi|33672140|gb|CF300379.1| 7LEAF--04-M01.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-M01,
mRNA sequence.
Length=40

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus


Query  1130   AATCTACCACCAA  1142
              |||||||||||||
Sbjct  40     AATCTACCACCAA  28
```


> ☐ gi|33672066|gb|CF300305.1| 7LEAF--04-K12.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-K12,
mRNA sequence.
Length=48

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus


Query  1130  AATCTACCACCAA  1142
             |||||||||||||               .
Sbjct  48    AATCTACCACCAA  36
```

> □ gi|33670844|gb|CF299083.1| 7LEAF--02-P01.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--02-P01,
mRNA sequence.
Length=50

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus


Query  1130  AATCTACCACCAA  1142
             |||||||||||||
Sbjct  50    AATCTACCACCAA  38
```

> □ gi|33669672|gb|CF297911.1| 7LEAF--01-B08.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-B08,
mRNA sequence.
Length=39

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus


Query  1130  AATCTACCACCAA  1142
             |||||||||||||
Sbjct  39    AATCTACCACCAA  27
```

> □ gi|26122450|gb|BQ592867.1| E012123-024-028-N11-SP6 MPIZ-ADIS-024-developing root Beta
cDNA clone 024-028-N11 5-PRIME, mRNA sequence.
Length=43

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 19/21 (90%), Gaps = 0/21 (0%)
 Strand=Plus/Minus


Query  1165  GCATTGGCTAAAGTTGACAAT  1185
             ||||||| | |||||||||||
Sbjct  40    GCATTGGTTCAAGTTGACAAT  20
```

> □ gi|20323261|dbj|AU258052.1| AU258052 3'-directed mouse cDNA library Mus musculus cDNA
BED0011943 3', mRNA sequence.
Length=23

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  268   GATCTTTCTTCTA   280
             |||||||||||||
Sbjct  1     GATCTTTCTTCTA   13
```

>☐ gi|13557556|dbj|AU108034.1| AU108034 Sugano Homo sapiens cDNA library Homo sapiens cDl
COL07140 5', mRNA sequence.
Length=50

```
 Score = 26.3 bits (13),  Expect =    15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  694   GCAGCAGCGGCTA   706
             |||||||||||||
Sbjct  9     GCAGCAGCGGCTA   21
```

>☐ gi|13555196|dbj|AU105675.1| AU105675 Sugano Homo sapiens cDNA library Homo sapiens cDl
HEP03089 5', mRNA sequence.
Length=50

```
 Score = 26.3 bits (13),  Expect =    15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  967   AAAACAGGAAGCA   979
             |||||||||||||
Sbjct  24    AAAACAGGAAGCA   12
```

```
 Score = 20.3 bits (10),  Expect =    916
 Identities = 10/10 (100%), Gaps = 0/10 (0%)
 Strand=Plus/Plus
```

```
Query  1084  GGTGGTAGCC   1093
             ||||||||||
Sbjct  29    GGTGGTAGCC   38
```

>☐ gi|13552589|dbj|AU103068.1| AU103068 Sugano Homo sapiens cDNA library Homo sapiens cDl
HSI02929 5', mRNA sequence.
Length=50

```
 Score = 26.3 bits (13),  Expect =    15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  79    GCAGCAGGTCAGG   91
             |||||||||||||
Sbjct  18    GCAGCAGGTCAGG   6
```

>☐ gi|13552582|dbj|AU103061.1| AU103061 Sugano Homo sapiens cDNA library Homo sapiens cDl
COLF1890 5', mRNA sequence.
Length=50

```
 Score = 26.3 bits (13),  Expect =    15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

Strand=Plus/Minus

```
Query  79   GCAGCAGGTCAGG   91
            |||||||||||||
Sbjct  28   GCAGCAGGTCAGG   16
```

>☐ gi|6071458|gb|AW100845.1| sd62b05.y1 Gm-c1008 Glycine max cDNA clone GENOME SYSTEMS CI
ID: Gm-c1008-874 5', mRNA sequence.
Length=49

 Score = 26.3 bits (13), Expect =   15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

```
Query  804  AATTGATGGTAAG   816
            |||||||||||||
Sbjct  28   AATTGATGGTAAG   16
```

>☐ gi|5425084|gb|AI813869.1| wk61b07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2419{
3' similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ;contains
MSR1.b2 MSR1 repetitive element ;, mRNA sequence.
Length=40

 Score = 26.3 bits (13), Expect =   15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

```
Query  653  ACACAAACATAGC   665
            |||||||||||||
Sbjct  1    ACACAAACATAGC   13
```

>☐ gi|3182248|gb|AA995759.1| os25e04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1606{
3' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN);,
mRNA sequence.
Length=35

 Score = 26.3 bits (13), Expect =   15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

```
Query  1063  ATGTATCTGAGCA   1075
             |||||||||||||
Sbjct  30    ATGTATCTGAGCA   18
```

 Score = 24.3 bits (12), Expect =   59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

```
Query  321  TGTATCTGAGCA   332
            ||||||||||||
Sbjct  29   TGTATCTGAGCA   18
```

>☐ gi|2217095|gb|AA486931.1| ab17b11.r1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:841053 5' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR

(HUMAN);, mRNA sequence.
Length=47

```
 Score = 26.3 bits (13),  Expect =     15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus


Query  320  GTGTATCTGAGCA  332
            |||||||||||||
Sbjct  18   GTGTATCTGAGCA  30



 Score = 24.3 bits (12),  Expect =     59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus


Query  1064  TGTATCTGAGCA  1075
             ||||||||||||
Sbjct  19    TGTATCTGAGCA  30
```

> ☐ gi|94359893|dbj|BY873732.1| BY873732 Germination shoots Hordeum vulgare subsp. vulgare
clone bast73f12 3', mRNA sequence.
Length=43

```
 Score = 24.3 bits (12),  Expect =     59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus


Query  604  AATGATATTTTT  615
            ||||||||||||
Sbjct  15   AATGATATTTTT  4
```

> ☐ gi|94351206|dbj|BY851751.1| BY851751 Germination shoots Hordeum vulgare subsp. vulgare
clone bast43c08 5', mRNA sequence.
Length=34

```
 Score = 24.3 bits (12),  Expect =     59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus


Query  23  GCTCCGCCATTG  34
           ||||||||||||
Sbjct  33  GCTCCGCCATTG  22
```

> ☐ gi|94344348|dbj|BY838005.1| BY838005 Etiolated seedling shoot Hordeum vulgare subsp. \
cDNA clone baet133e11 5', mRNA sequence.
Length=34

```
 Score = 24.3 bits (12),  Expect =     59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus


Query  759  AACAACTGCAGC  770
            ||||||||||||
Sbjct  5    AACAACTGCAGC  16
```

>☐ gi|93276160|gb|EB651462.1| GmUSCLM04pTriplEx216i23f1 Gillichthys liver & muscle librar
2 Gillichthys mirabilis cDNA clone 16i23 5', mRNA sequence.
Length=41

 Score = 24.3 bits (12), Expect =   59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 1135   ACCACCAACCCG   1146
              ||||||||||||
Sbjct 17   ACCACCAACCCG   28

>☐ gi|90038657|emb|CT579987.1| CT579987 LG0ACA Pinus pinaster cDNA, mRNA sequence.
Length=50

 Score = 24.3 bits (12), Expect =   59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 42   CTCTTCTGGCCT   53
            ||||||||||||
Sbjct 25   CTCTTCTGGCCT   36

>☐ gi|86584902|gb|DY249267.1| CSTFB1E0092A_78_127 CST-ProHSC Mus musculus cDNA, mRNA sequ
Length=49

 Score = 24.3 bits (12), Expect =   59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 788   GTGTATATTCTG   799
             ||||||||||||
Sbjct 17   GTGTATATTCTG   6

>☐ gi|86581169|gb|DY245525.1| CSTBQ1D1085A_697_744 CST-BM Mus musculus cDNA, mRNA sequenc
Length=47

 Score = 24.3 bits (12), Expect =   59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 4   AAATCTCAGTCT   15
           ||||||||||||
Sbjct 11   AAATCTCAGTCT   22

>☐ gi|86580675|gb|DY245031.1| CSTBQ1D0814A_96_144 CST-BM Mus musculus cDNA, mRNA sequence
Length=48

 Score = 24.3 bits (12), Expect =   59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 71   AAGATGACGCAG   82

```
            ||||||||||||
Sbjct  45   AAGATGACGCAG   34
```

>□gi|86578949|gb|DY243305.1| CSTBQ1D0006A_0_33 CST-BM Mus musculus cDNA, mRNA sequence.
Length=33

```
 Score = 24.3 bits (12),  Expect =    59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  114   AAATATTAAAGG   125
             ||||||||||||
Sbjct  2     AAATATTAAAGG   13
```

>□gi|82578105|gb|DV749761.1| ID0AAH2BH05ZM1 ID0AAH Acyrthosiphon pisum cDNA clone ID0AAH
5', mRNA sequence.
Length=38

```
 Score = 24.3 bits (12),  Expect =    59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query  396   TAATGATGGTGA   407
             ||||||||||||
Sbjct  20    TAATGATGGTGA   9
```

>□gi|77991981|gb|DV467808.1| est_t_truncatus843 HML_TuTr_IL-2 Tursiops truncatus cDNA, n
sequence.
Length=18

```
 Score = 24.3 bits (12),  Expect =    59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query  1044   TTCTGGTAACAA   1055
              ||||||||||||
Sbjct  15     TTCTGGTAACAA   4
```

>□gi|77597704|gb|DV228503.1| EST-AR183A10 Infected Porcine Peripheral Blood Cell cDNA 1:
Sus scrofa cDNA clone AR183A10, mRNA sequence.
Length=48

```
 Score = 24.3 bits (12),  Expect =    59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  358   CTTGCTGAAAAT   369
             ||||||||||||
Sbjct  30    CTTGCTGAAAAT   41
```

>□gi|77498900|gb|DV212698.1| 0089P0174Z_H04_T7 Mimulus guttatus library 2 Mimulus guttat
cDNA clone 0089P0174Z_H04 5', mRNA sequence.
Length=34

```
 Score = 24.3 bits (12),   Expect =     59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  370   AATGAAATGAAA   381
             ||||||||||||
Sbjct  17    AATGAAATGAAA   28


 Score = 20.3 bits (10),   Expect =    916
 Identities = 10/10 (100%), Gaps = 0/10 (0%)
 Strand=Plus/Plus

Query  191   TGAATGAAAT   200
             ||||||||||
Sbjct  15    TGAATGAAAT   24
```

> □ gi|75475804|emb|AM075317.1| AM075317 Chicken immune 2 - CSEQRBN29 Gallus gallus cDNA c
C0000466A11_T7, mRNA sequence.
Length=20

```
 Score = 24.3 bits (12),   Expect =     59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  621   TGCAGCAGATGG   632
             ||||||||||||
Sbjct  1     TGCAGCAGATGG   12
```

> □ gi|86027041|gb|DR322794.1| 143010 CERES-148 Arabidopsis thaliana cDNA clone 111205 5',
sequence.
Length=50

```
 Score = 24.3 bits (12),   Expect =     59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  960   AGCTAAGAAAAC   971
             ||||||||||||
Sbjct  20    AGCTAAGAAAAC   31
```

> □ gi|85905326|gb|DR226284.1| 5735955 CERES-AL46 Arabidopsis thaliana cDNA clone 1143515
mRNA sequence.
Length=50

```
 Score = 24.3 bits (12),   Expect =     59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  37    CGTCTCTCTTCT   48
             ||||||||||||
Sbjct  16    CGTCTCTCTTCT   27
```

> □ gi|67567668|gb|DR108313.1| JHU161B11L41 Canine cardiovascular system biased cDNA Canis

cDNA, mRNA sequence.
Length=41

```
 Score = 24.3 bits (12),  Expect =    59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query  607   GATATTTTTGTT  618
             ||||||||||||
Sbjct  5     GATATTTTTGTT  16
```

> ☐ gi|75922290|gb|AR703977.1| Sequence 7 from patent US 6929909
Length=18

  Score = 32.2 bits (16), Expect = 2.9
  Identities = 16/16 (100%), Gaps = 0/16 (0%)
  Strand=Plus/Minus

Query 796   TCTGCAGAAATTGATG   811
             ||||||||||||||||
Sbjct 17   TCTGCAGAAATTGATG   2

> ☐ gi|42687870|gb|AR454420.1| Sequence 5 from patent US 6682741
Length=24

  Score = 32.2 bits (16), Expect = 2.9
  Identities = 16/16 (100%), Gaps = 0/16 (0%)
  Strand=Plus/Minus

Query 354   AGTCCTTGCTGAAAAT   369
             ||||||||||||||||
Sbjct 16   AGTCCTTGCTGAAAAT   1

> ☐ gi|33751074|gb|AR350119.1| Sequence 58 from patent US 6586229
Length=24

  Score = 32.2 bits (16), Expect = 2.9
  Identities = 16/16 (100%), Gaps = 0/16 (0%)
  Strand=Plus/Minus

Query 977   GCACGTTAGTTGTTAA   992
             ||||||||||||||||
Sbjct 23   GCACGTTAGTTGTTAA   8

> ☐ gi|92250878|dbj|BD359459.1| Process for the production of UDP-glucronic acid
Length=30

  Score = 32.2 bits (16), Expect = 2.9
  Identities = 16/16 (100%), Gaps = 0/16 (0%)
  Strand=Plus/Minus

Query 545   TTGGCGGTGATGCTTA   560
             ||||||||||||||||
Sbjct 26   TTGGCGGTGATGCTTA   11

> ☐ gi|92244643|dbj|BD342484.1| Novel ubiquitin specific proteases
Length=33

  Score = 32.2 bits (16), Expect = 2.9
  Identities = 16/16 (100%), Gaps = 0/16 (0%)
  Strand=Plus/Minus

Query 1236   CAACCTTGGCAACACC   1251
              ||||||||||||||||
Sbjct 33   CAACCTTGGCAACACC   18

> ☐ gi|92244642|dbj|BD342483.1| Novel ubiquitin specific proteases
Length=33

 Score = 32.2 bits (16), Expect = 2.9
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 1236   CAACCTTGGCAACACC   1251
              ||||||||||||||||
Sbjct 1   CAACCTTGGCAACACC   16

> ☐ gi|21901300|emb|AX468464.1| Sequence 7 from Patent WO0222834
Length=18

 Score = 32.2 bits (16), Expect = 2.9
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 796   TCTGCAGAAATTGATG   811
             ||||||||||||||||
Sbjct 17   TCTGCAGAAATTGATG   2

> ☐ gi|27949121|emb|AX590489.1| Sequence 1 from Patent WO02085933
Length=36

 Score = 32.2 bits (16), Expect = 2.9
 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 1201   GGTGCAGTACAAAACCGTTTCGACTCTGCTAT   1232
              ||||| ||||| |||||||||| |||| |||||
Sbjct 1   GGTGCGGTACAGAACCGTTTCAACTCCGCTAT   32

> ☐ gi|18093617|emb|AX322597.1| Sequence 58 from Patent WO0192539
Length=24

 Score = 32.2 bits (16), Expect = 2.9
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 977   GCACGTTAGTTGTTAA   992
             ||||||||||||||||
Sbjct 23   GCACGTTAGTTGTTAA   8

> ☐ gi|18622154|dbj|E50954.1| Process for preparing Escherichia coli H antigen
Length=20

 Score = 32.2 bits (16), Expect = 2.9
 Identities = 19/20 (95%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

Query 118   ATTAAAGGTCTGACTCAGGC   137

```
              |||||||| |||||||||||
Sbjct  1      ATTAAAGGCCTGACTCAGGC   20
```

> ☐ gi|56657472|gb|AR605808.1| Sequence 615 from patent US 6818751
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

```
Query  451    GGCCTGGACGGTTTT   465
              |||||||||||||||
Sbjct  25     GGCCTGGACGGTTTT   39
```

> ☐ gi|56657468|gb|AR605804.1| Sequence 611 from patent US 6818751
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

```
Query  451    GGCCTGGACGGTTTT   465
              |||||||||||||||
Sbjct  22     GGCCTGGACGGTTTT   8
```

> ☐ gi|56635885|gb|AR588988.1| Sequence 615 from patent US 6800746
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

```
Query  451    GGCCTGGACGGTTTT   465
              |||||||||||||||
Sbjct  25     GGCCTGGACGGTTTT   39
```

> ☐ gi|56635881|gb|AR588984.1| Sequence 611 from patent US 6800746
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

```
Query  451    GGCCTGGACGGTTTT   465
              |||||||||||||||
Sbjct  22     GGCCTGGACGGTTTT   8
```

> ☐ gi|77365703|gb|AR717054.1| Sequence 615 from patent US 6943236
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

```
Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  25    GGCCTGGACGGTTTT   39
```

> ☐ gi|77365699|gb|AR717050.1| Sequence 611 from patent US 6943236
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%),  Gaps = 0/15 (0%)
 Strand=Plus/Minus
```

```
Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  22    GGCCTGGACGGTTTT   8
```

> ☐ gi|53979053|gb|AR564002.1| Sequence 615 from patent US 6759515
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%),  Gaps = 0/15 (0%)
 Strand=Plus/Plus
```

```
Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  25    GGCCTGGACGGTTTT   39
```

> ☐ gi|53979049|gb|AR563998.1| Sequence 611 from patent US 6759515
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%),  Gaps = 0/15 (0%)
 Strand=Plus/Minus
```

```
Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  22    GGCCTGGACGGTTTT   8
```

> ☐ gi|40154459|gb|AR405622.1| Sequence 615 from patent US 6630305
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%),  Gaps = 0/15 (0%)
 Strand=Plus/Plus
```

```
Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  25    GGCCTGGACGGTTTT   39
```

> ☐ gi|40154455|gb|AR405618.1| Sequence 611 from patent US 6630305
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
```

```
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  451  GGCCTGGACGGTTTT  465
            |||||||||||||||
Sbjct   22  GGCCTGGACGGTTTT    8
```

> ☐ gi|40143650|gb|AR400355.1| Sequence 615 from patent US 6620922
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  451  GGCCTGGACGGTTTT  465
            |||||||||||||||
Sbjct   25  GGCCTGGACGGTTTT   39
```

> ☐ gi|40143642|gb|AR400351.1| Sequence 611 from patent US 6620922
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  451  GGCCTGGACGGTTTT  465
            |||||||||||||||
Sbjct   22  GGCCTGGACGGTTTT    8
```

> ☐ gi|74474231|emb|CS159058.1| Sequence 17 from Patent WO2005080576
Length=25

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  743  GAGTTGAATTCACAA  757
            |||||||||||||||
Sbjct   17  GAGTTGAATTCACAA    3
```

> ☐ gi|23320295|gb|AR219325.1| Sequence 56 from patent US 6420157
Length=30

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  451  GGCCTGGACGGTTTT  465
            |||||||||||||||
Sbjct   14  GGCCTGGACGGTTTT   28
```

> ☐ gi|61890282|emb|CS051099.1| Sequence 24 from Patent WO2005021740
Length=25

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  743   GAGTTGAATTCACAA   757
             |||||||||||||||
Sbjct  17    GAGTTGAATTCACAA   3
```

> ☐gi|92345575|dbj|BD398016.1| COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF
CANCER
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  25    GGCCTGGACGGTTTT   39
```

> ☐gi|92345571|dbj|BD398012.1| COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF
CANCER
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  22    GGCCTGGACGGTTTT   8
```

> ☐gi|92331562|dbj|BD397081.1| DNA Encoding a Novel Prost 07 Polypeptide
Length=30

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  16    GGCCTGGACGGTTTT   30
```

> ☐gi|60730322|emb|CS029344.1| Sequence 17 from Patent EP1510585
Length=25

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  743   GAGTTGAATTCACAA   757
             |||||||||||||||
Sbjct  17    GAGTTGAATTCACAA   3
```

> ☐ gi|60730290|emb|CS029312.1| Sequence 24 from Patent EP1510573
Length=25

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 743 GAGTTGAATTCACAA 757
            |||||||||||||||
Sbjct 17   GAGTTGAATTCACAA 3

> ☐ gi|92320083|dbj|BD437481.1| PROSTASE PROTEIN VACCINE COMPRISING DERIVATISED THIOL RES:
AND METHODS FOR PRODUCING SAID ANTIGEN
Length=30

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 451 GGCCTGGACGGTTTT 465
            |||||||||||||||
Sbjct 13   GGCCTGGACGGTTTT 27

> ☐ gi|92289859|dbj|BD444719.1| COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF
CANCER
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 451 GGCCTGGACGGTTTT 465
            |||||||||||||||
Sbjct 25   GGCCTGGACGGTTTT 39

> ☐ gi|92289855|dbj|BD444715.1| COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF
CANCER
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 451 GGCCTGGACGGTTTT 465
            |||||||||||||||
Sbjct 22   GGCCTGGACGGTTTT 8

> ☐ gi|29712869|gb|AR278623.1| Sequence 615 from patent US 6512094
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

```
Query  451  GGCCTGGACGGTTTT  465
            |||||||||||||||
Sbjct  25   GGCCTGGACGGTTTT  39
```

> ☐ gi|29712865|gb|AR278619.1| Sequence 611 from patent US 6512094
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus
```

```
Query  451  GGCCTGGACGGTTTT  465
            |||||||||||||||
Sbjct  22   GGCCTGGACGGTTTT  8
```

> ☐ gi|67590289|gb|AR657147.1| Sequence 615 from patent US 6894146
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus
```

```
Query  451  GGCCTGGACGGTTTT  465
            |||||||||||||||
Sbjct  25   GGCCTGGACGGTTTT  39
```

> ☐ gi|67590285|gb|AR657143.1| Sequence 611 from patent US 6894146
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus
```

```
Query  451  GGCCTGGACGGTTTT  465
            |||||||||||||||
Sbjct  22   GGCCTGGACGGTTTT  8
```

> ☐ gi|44845533|emb|CQ754277.1| Sequence 15 from Patent WO2004001069
Length=20

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus
```

```
Query  621  TGCAGCAGATGGTTC  635
            |||||||||||||||
Sbjct  1    TGCAGCAGATGGTTC  15
```

> ☐ gi|10025691|gb|AR096679.1|AR096679 Sequence 17 from patent US 6008193
Length=37

```
 Score = 30.2 bits (15),  Expect =    11
```

```
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus


Query  65  GTGCTAAAGATGACG  79
           |||||||||||||||
Sbjct  6   GTGCTAAAGATGACG  20
```

> ☐ gi|41014894|emb|CQ008203.1| Sequence 6843 from Patent WO0147944
Length=50

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 Score = 30.2 bits (15),  Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  1304  CCGAAGTGTCTAACA  1318
             |||||||||||||||
Sbjct  18    CCGAAGTGTCTAACA  4
```

> ☐ gi|39722415|emb|AX816969.1| Sequence 12 from Patent WO03068819
Length=47

```
 Score = 30.2 bits (15),  Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  467  ATATCGATGGCGCGC  481
            |||||||||||||||
Sbjct  22   ATATCGATGGCGCGC  36
```

> ☐ gi|21694924|emb|AX446025.1| Sequence 2480 from Patent WO0216649
Length=24

```
 Score = 30.2 bits (15),  Expect =   11
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus


Query  535  AACTATGATGTTGGCGGTG  553
            ||||||||| |||||||||
Sbjct  22   AACTATGAGGTTGGCGGTG  4
```

> ☐ gi|22205164|emb|AX469891.1| Sequence 8 from Patent WO02053771
Length=22

```
 Score = 30.2 bits (15),  Expect =   11
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Plus


Query  358  CTTGCTGAAAATAATGAAA  376
            |||||||||| ||||||||
Sbjct  3    CTTGCTGAAAAAAATGAAA  21
```

> ☐ gi|33036418|dbj|BD226648.1| Use of antiprolactin agent for remedy of hypercytosis
Length=20

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  753   CACAACAACAACTGC   767
             |||||||||||||||
Sbjct  20    CACAACAACAACTGC   6
```


> ☐ gi|33036413|dbj|BD226643.1| Use of antiprolactin agent for remedy of hypercytosis
Length=20

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus


Query  753   CACAACAACAACTGC   767
             |||||||||||||||
Sbjct  20    CACAACAACAACTGC   6
```


> ☐ gi|32949314|emb|AX781460.1| Sequence 12 from Patent EP1321477
Length=47

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  467   ATATCGATGGCGCGC   481
             |||||||||||||||
Sbjct  22    ATATCGATGGCGCGC   36
```


> ☐ gi|15863084|emb|AX248461.1| Sequence 540 from Patent WO0166800
Length=31

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  1109   AAGATGCAGCAAAAT   1123
              |||||||||||||||
Sbjct  1      AAGATGCAGCAAAAT   15
```


> ☐ gi|16516314|emb|AX267641.1| Sequence 615 from Patent WO0173032
Length=46

```
 Score = 30.2 bits (15),  Expect =    11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus


Query  451   GGCCTGGACGGTTTT   465
             |||||||||||||||
Sbjct  25    GGCCTGGACGGTTTT   39
```

> ☐ gi|16516310|emb|AX267637.1| Sequence 611 from Patent WO0173032
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 451 GGCCTGGACGGTTTT 465
            |||||||||||||||
Sbjct 22   GGCCTGGACGGTTTT 8

> ☐ gi|15390812|emb|AX200985.1| Sequence 615 from Patent WO0151633
Length=46

 Score = 30.2 bits (15), Expect =   11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 451 GGCCTGGACGGTTTT 465
            |||||||||||||||
Sbjct 25   GGCCTGGACGGTTTT 39.